

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	834	59.1	834	6	BD141394	BD141394 Novel car
	2	437.4	31.0	110000	1	AP006840_07	Continuation (8 of
	3	372.4	26.4	341887	1	AP003006	AP003006 Mesorhizo
c	4	366	26.0	299425	1	AP005049	AP005049 Streptomy
	5	344.8	24.5	294800	1	SME591789	AL591789 Sinorhizo
	6	340.4	24.1	110000	1	BX571965_10	Continuation (11 o
	7	339.8	24.1	10386	1	AE004515	AE004515 Pseudomon
c	8	338.8	24.0	110000	1	CP000010_23	Continuation (24 o
	9	335.8	23.8	822	12	AY658815	AY658815 Synthetic
	10	317.2	22.5	310967	1	AE016869	AE016869 Pseudomon
c	11	315.6	22.4	300395	1	AE016785	AE016785 Pseudomon
	12	310.8	22.0	1084	6	AX477714	AX477714 Sequence
	13	293.8	20.8	10325	1	AE009154	AE009154 Agrobacte

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1455	100.0	277	5	AAO16951	Aao16951 M luteus
2	871	59.9	281	8	ADS23099	Ads23099 Bacterial
3	812	55.8	352	7	ABO80918	Abo80918 Pseudomon
4	810	55.7	277	8	ADS22524	Ads22524 Bacterial
5	806	55.4	281	6	ABU22187	Abu22187 Protein e
6	783	53.8	266	8	ADS25492	Ads25492 Bacterial
7	783	53.8	266	8	ADS25964	Ads25964 Bacterial
8	783	53.8	266	8	ADS25281	Ads25281 Bacterial
9	777	53.4	276	8	ADN25959	Adn25959 Bacterial
10	774	53.2	273	8	ADS25018	Ads25018 Bacterial
11	772	53.1	281	6	ABU21692	Abu21692 Protein e
12	765	52.6	273	5	AAE25028	Aae25028 Human dru
13	752	51.7	284	8	ADN18215	Adn18215 Bacterial
14	749	51.5	273	6	ABU41426	Abu41426 Protein e
15	706	48.5	256	8	ADN24621	Adn24621 Bacterial
16	706	48.5	256	8	ADN21862	Adn21862 Bacterial
17	686.5	47.2	324	7	ABO61379	Abo61379 Klebsiell
18	682.5	46.9	265	8	ADS30915	Ads30915 Bacterial
19	656	45.1	275	8	ADS30423	Ads30423 Bacterial

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1410	100.0	1410	6	AAL45070	Aal45070 M luteus
2	834	59.1	834	6	AAL45071	Aal45071 M luteus
3	370.8	26.3	846	13	ADS60145	Ads60145 Bacterial
4	347.8	24.7	843	8	ACA25562	Aca25562 Prokaryot
5	346.2	24.6	1059	11	ABD14489	Abd14489 Pseudomon
6	334.8	23.7	843	8	ACA26057	Aca26057 Prokaryot
7	333.8	23.7	828	13	ADS56625	Ads56625 Bacterial
8	324.4	23.0	768	13	ADS49772	Ads49772 Bacterial
9	324.4	23.0	768	13	ADS55287	Ads55287 Bacterial
10	316.8	22.5	819	13	ADS62064	Ads62064 Bacterial
11	314.2	22.3	819	8	ACA45296	Aca45296 Prokaryot
12	310.8	22.0	1084	6	AAD40577	Aad40577 Human dru
13	290.4	20.6	831	13	ADS59570	Ads59570 Bacterial
14	285.6	20.3	798	13	ADS63010	Ads63010 Bacterial
15	285.6	20.3	798	13	ADS62327	Ads62327 Bacterial
16	285.6	20.3	798	13	ADS62538	Ads62538 B

Title: US-10-088-920A-2
 Perfect score: 1410
 Sequence: 1 ggtacccgcccgcctcctat.....tcgaggaaggaacggagctc 1410

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	346.2	24.6	1059	4	US-09-252-991A-13093	Sequence 13093, A
2	288	20.4	21330	4	US-09-902-540-1209	Sequence 1209, Ap
c 3	282.6	20.0	681	4	US-09-252-991A-12847	Sequence 12847, A
4	281.4	20.0	819	4	US-09-902-540-4212	Sequence 4212, Ap
5	226.2	16.0	975	4	US-09-489-039A-725	Sequence 725, App
c 6	217	15.4	564	4	US-09-252-991A-12700	Sequence 12700, A
c 7	154.2	10.9	438	4	US-09-489-039A-666	Sequence 666, App
c 8	92.4	6.6	2031	4	US-09-634-238-129	Sequence 129, App
9	82	5.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
10	82	5.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
11	81	5.7	1077	4	US-09-252-991A-14964	Sequence 14964, A

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	1410	100.0	1410	16	US-10-088-920A-2
2	370.8	26.3	846	17	US-10-369-493-35819
c 3	366	26.0	9025608	15	US-10-156-761-1
4	363.6	25.8	843	15	US-10-156-761-7212
5	347.8	24.7	843	17	US-10-282-122A-13432
6	334.8	23.7	843	17	US-10-282-122A-13927
7	333.8	23.7	828	17	US-10-369-493-32299
8	324.4	23.0	768	17	US-10-369-493-28202
9	324.4	23.0	768	17	US-10-369-493-30961

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_htc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						Description
	No.	Score	Match	Length	DB	ID	
c	1	169.6	12.0	929	8	BZ570067	BZ570067 msh2_115.
	2	120.8	8.6	608	9	CG913045	CG913045 ZMMBBb037
c	3	119.6	8.5	812	9	BX908536	BX908536 Leishmani
c	4	80.2	5.7	1516	4	BG809984	BG809984 mgct002xd
	5	79.2	5.6	458	8	AQ868055	AQ868055 nbeb0017D
	6	78.6	5.6	1516	4	BG809984	BG809984 mgct002xd
	7	78.4	5.6	1821	9	CL090560	CL090560 ISB1-17N1
c	8	76.2	5.4	1780	9	AG448243	AG448243 Mus muscu
c	9	76	5.4	1131	9	AG042920	AG042920 Pan trogl
	10	75	5.3	457	8	BZ895098	BZ895098 Hg7_0124
	11	73.8	5.2	1780	9	AG448243	AG448243 Mus muscu
c	12	73.2	5.2	1798	9	AG171124	AG171124 Pan trogl
	13	73	5.2	925	9	CNS0091P	AL053013 Drosophil
c	14	72.8	5.2	925	9	CNS0091P	AL053013 Drosophil
	15	72	5.1	462	5	BQ640772	BQ640772 TVEST004.
	16	71.2	5.0	984	8	BZ560840	BZ560840 pacs2-164
	17	70.2	5.0	2483	9	CL496067	CL496067 SAIL_619_
c	18	69.8	5.0	1821	9	CL090560	CL090560 ISB1-17N1
	19	69.6	4.9	2243	9	AG381986	AG381986 Mus muscu

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	812	55.8	352	4	US-09-252-991A-29664	Sequence 29664, A	
2	686.5	47.2	324	4	US-09-489-039A-7896	Sequence 7896, Ap	
3	568	39.0	240	4	US-09-902-540-11508	Sequence 11508, A	
4	346.5	23.8	358	4	US-09-252-991A-31535	Sequence 31535, A	
5	337	23.2	306	4	US-09-902-540-9859	Sequence 9859, Ap	
6	329.5	22.6	350	4	US-09-489-039A-9552	Sequence 9552, Ap	
7	318.5	21.9	328	4	US-09-489-039A-12803	Sequence 12803, A	
8	308.5	21.2	292	4	US-09-489-039A-12672	Sequence 12672, A	
9	307	21.1	291	4	US-09-107-532A-5063	Sequence 5063, Ap	
10	300	20.6	314	4	US-09-902-540-14628	Sequence 14628, A	
11	298.5	20.5	330	4	US-09-724-797-28	Sequence 28, Appl	
12	297.5	20.4	332	4	US-09-107-532A-6891	Sequence 6891, Ap	
13	297	20.4	243	4	US-09-134-000C-6794	Sequence 6794, Ap	
14	294.5	20.2	321	4	US-09-489-039A-13361	Sequence 13361, A	
15	291.5	20.0	348	4	US-09-673-198-4	Sequence 4, Appli	
16	291	20.0	298	4	US-09-134-000C-6059	Sequence 6059, Ap	
17	288.5	19.8	316	1	US-08-585-595-3	Sequence 3, Appli	
18	288	19.8	330	4	US-09-679-279-10	Sequence 10, Appl	
19	288	19.8	351	4	US-09-489-039A-11976	Sequence 11976, A	
20	287.5	19.8	351	4	US-09-252-991A-19370	Sequence 19370, A	
21	284.5	19.6	316	3	US-08-801-344-4	Sequence 4, Appli	
22	284.5	19.6	316	3	US-09-498-599-4	Sequence 4, Appli	
23	283.5	19.5	279	4	US-09-543-681A-7803	Sequence 7803, Ap	
24	280	19.2	341	4	US-09-252-991A-30076	Sequence 30076, A	
25	279.5	19.2	334	4	US-09-328-352-6079	Sequence 6079, Ap	
26	276.5	19.0	290	4	US-09-248-796A-17316	Sequence 17316, A	

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	1455	100.0		277	14	US-10-088-920A-1	Sequence 1, Appli
2	881.5	60.6		281	14	US-10-156-761-14762	Sequence 14762, A
3	871	59.9		281	15	US-10-369-493-12132	Sequence 12132, A
4	810	55.7		277	15	US-10-369-493-11557	Sequence 11557, A
5	806	55.4		281	15	US-10-282-122A-50111	Sequence 50111, A
6	783	53.8		266	15	US-10-369-493-14314	Sequence 14314, A
7	783	53.8		266	15	US-10-369-493-14525	Sequence 14525, A
8	783	53.8		266	15	US-10-369-493-14997	Sequence 14997, A
9	777	53.4		276	15	US-10-369-493-8612	Sequence 8612, Ap.
10	774	53.2		273	15	US-10-369-493-14051	Sequence 14051, A

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	810	55.7	281	2	A97604	probable oxidoredu
2	810	55.7	281	2	AB2826	aldo/keto reductas
3	803	55.2	273	2	A83546	probable oxidoredu
4	752	51.7	284	1	E64938	probable aldehyde
5	749	51.5	284	2	F85788	probable an aldehy
6	749	51.5	284	2	B90940	probable an aldehy
7	723.5	49.7	285	2	AI0711	probable oxidoredu
8	486	33.4	274	2	F72218	oxidoreductase, al
9	448.5	30.8	273	2	D71221	probable morphine
10	441.5	30.3	279	2	F75188	morphine 6-dehydro
11	416	28.6	292	2	B90454	dehydrogenase [imp
12	400	27.5	319	2	AH2062	aldo/keto reductas
13	396.5	27.3	265	2	B90506	oxidoreductase, al
14	375.5	25.8	277	2	B84205	aldehyde reductase
15	362.5	24.9	354	2	T44934	mocA protein [impo
16	351	24.1	304	2	H90466	oxidoreductase [im
17	346.5	23.8	331	2	H83328	probable oxidoredu
18	345.5	23.7	294	2	AC3642	2,5-diketo-D-gluc
19	344.5	23.7	348	2	AB3121	oxidoreductase moc
20	344.5	23.7	395	2	E98166	mocA protein [impo
21	344	23.6	331	2	B95902	probable aldoketo
22	340.5	23.4	276	2	C70040	plant-metabolite d
23	340	23.4	276	2	F83919	plant-metabolite d
24	335	23.0	278	2	A84131	plant-metabolite d
25	332	22.8	329	2	AG0519	probable aldo/keto
26	324.5	22.3	314	2	S75995	hypothetical prote
27	324	22.3	280	2	D69988	plant metabolite d
28	324	22.3	332	2	D98252	general stress pro

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	957	65.8	280	2	Q67RQ0	Q67rq0 symbiobacte
2	881.5	60.6	281	2	Q826G0	Q826g0 streptomyce
3	871	59.9	281	2	Q98C22	Q98c22 rhizobium l
4	810	55.7	281	2	Q8UDT7	Q8udt7 agrobacteri
5	807	55.5	281	2	Q63WJ9	Q63wj9 burkholderi
6	806	55.4	281	2	Q62HK0	Q62hk0 burkholderi
7	805	55.3	281	2	Q92NR7	Q92nr7 rhizobium m
8	803	55.2	273	2	Q9I5D4	Q9i5d4 pseudomonas
9	754	51.8	299	2	Q8FGW6	Q8fgw6 escherichia
10	752	51.7	284	1	YEAE_ECOLI	P76234 escherichia
11	749	51.5	273	2	Q87YU2	Q87yu2 pseudomonas
12	749	51.5	284	2	Q8XDT9	Q8xdt9 escherichia
13	742.5	51.0	253	2	Q88I81	Q88i81 pseudomonas
14	725.5	49.9	283	2	Q6D4P4	Q6d4p4 erwinia car
15	724.5	49.8	285	2	Q8ZPW0	Q8zpw0 salmonella
16	723.5	49.7	285	2	Q8Z6F0	Q8z6f0 salmonella
17	671.5	46.2	286	2	Q89RG2	Q89rg2 bradyrhizob
18	663.5	45.6	253	2	Q7UCK6	Q7uck6 shigella fl
19	662.5	45.5	253	2	Q83RH8	Q83rh8 shigella fl
20	658.5	45.3	277	2	Q6N7V4	Q6n7v4 rhodopseudo
21	635.5	43.7	284	2	Q8PBK9	Q8pbk9 xanthomonas
22	630.5	43.3	281	2	Q7WAQ1	Q7waq1 bordetella
23	630.5	43.3	284	2	Q8PN61	Q8pn61 xanthomonas
24	623.5	42.9	281	2	Q7WJV6	Q7wvjv6 bordetella
25	597	41.0	279	2	Q74HC5	Q74hc5 lactobacill
26	532	36.6	256	2	Q9Z657	Q9z657 zymomonas m
27	525	36.1	283	2	Q65UR6	Q65ur6 mannheimia